N -
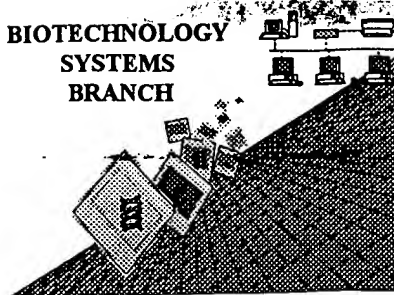
RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information #6
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _09/545,199A_

Source: _1643_

Date Processed by STIC: _10/2/2000_

RECEIVED

OCT 13 2000

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY
EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT
   COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY
   or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT,
   WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER,
703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program
employing a logical and intuitive user-interface to check whether a sequence listing is in
compliance with format and content rules. Checker Version 3.0 works for sequence listings
generated for the original version of 37 CFR §§1.821-1.825 effective October 1, 1990 (old
rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual
Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-
compliant. Checker allows public users to check sequence listings in Computer Readable form
(CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence
listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Application No.: 09/545,199

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other: _____

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support (SIRA)
     Technical Assistance..703-287-0200
     To Purchase PatentIn Software.......................703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/545,199A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1643

RAW SEQUENCE LISTING   DATE: 10/02/2000
PATENT APPLICATION: US/09/545,199A   TIME: 15:58:32

Input Set : A:\6227.txt
Output Set: N:\CRF3\10022000\I545199A.raw

Does Not Comply
Corrected Diskette Needed

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 4 <110> APPLICANT: Lowery E., David
 5          Fuller E., Troy
 6          Kennedy J., Michael
 8 <120> TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
10 <130> FILE REFERENCE: 28341/6227.1
12 <140> CURRENT APPLICATION NUMBER: US/09/545,199A
13 <141> CURRENT FILING DATE: 2000-04-06
15 <150> PRIOR APPLICATION NUMBER: 60/153,453
16 <151> PRIOR FILING DATE: 1999-09-10
18 <150> PRIOR APPLICATION NUMBER: 60/128,689
19 <151> PRIOR FILING DATE: 1999-04-09
21 <160> NUMBER OF SEQ ID NOS: 165
23 <170> SOFTWARE: PatentIn Ver. 2.0
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ERRORED SEQUENCES

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1978 <210> SEQ ID NO: 16
1979 <211> LENGTH: 2110
1980 <212> TYPE: PRT
1981 <213> ORGANISM: Pasteurella multocida
1983 <400> SEQUENCE: 16
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1985  1               5                  10                  15
1987 Gln Glu Asn Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala
1988             20                  25                  30
1990 Glu Arg Ser Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu
1991         35                  40                  45
1993 Thr Val His Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn
1994        50                  55                  60
1996 Val Ser Tyr Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg
1997 65                  70                  75                  80
1999 Val Ala Val His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn
2000                 85                  90                  95
2002 Leu Gln Glu Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala
2003             100                 105                 110
2005 Ile Arg Ser Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser
2006        115                 120                 125
2008 Ser Glu Ser Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys
2009    130                 135                 140
2011 Gly Thr Phe Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala
2012 145                 150                 155                 160
2014 Phe Asn Gln Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile
2015                 165                 170                 175
2017 Thr Met Tyr Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser
2018            180                 185                 190
2020 Gly Asn Ala Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala
```

```
2021          195                    200                  205
2023 Leu Phe Gly Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu
2024       210                   215                  220
2026 Asn Phe Ser Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met
2027 225                   230                   235                  240
2029 Tyr Gln Lys Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys
2030                   245                   250                  255
2032 Ser Tyr Asp Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro
2033             260                   265                  270
2035 Thr Asp Phe Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly
2036       275                   280                  285
2038 Lys Leu Glu Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu
2039       290                   295                  300
2041 Arg Gly Lys Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser
2042 305                   310                  315                  320
2044 Leu Pro Ser Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu
2045                   325                   330                  335
2047 Glu Glu Asp Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met
2048             340                   345                  350
2050 Pro Asn Leu Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu
2051       355                   360                  365
2053 Ser Pro Ile Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile
2054       370                   375                  380
2056 Glu Glu Ser His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp
2057 385                   390                  395                  400
2059 Asp Glu Ser Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu
2060             405                   410                  415
2062 Lys Glu Met Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly
2063             420                   425                  430
2065 Asn Lys Pro Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp
2066       435                   440                  445
2068 Glu Phe Phe Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu
2069       450                   455                  460
2071 Gly Glu Glu Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser
2072 465                   470                  475                  480
2074 Thr Asn Leu Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys
2075             485                   490                  495
2077 Arg Glu Lys Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys
2078             500                   505                  510
2080 Leu Gln Glu Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln
2081       515                   520                  525
2083 Lys Ala Arg Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu
2084       530                   535                  540
2086 Lys Arg Val Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp
2087 545                   550                  555                  560
2089 Lys Ile Ala Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu
2090             565                   570                  575
2092 Glu Ile Arg Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu
2093             580                   585                  590
```

```
2095 Glu Lys Lys Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln
2096         595             600             605
2098 Ala Glu Gln Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu
2099     610             615             620
2101 Asp Ile Glu Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala
2102 625             630             635             640
2104 Glu Ala Ser Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro
2105             645             650             655
2107 Lys Val Glu Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn
2108         660             665             670
2110 Gln Asp Asp Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu
2111     675             680             685
2113 Asn Thr Lys Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe
2114     690             695             700
2116 Asp His Gln Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His
2117 705             710             715             720
2119 Leu Asn Gln Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu
2120             725             730             735
2122 Met Asp Asn Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly
2123             740             745             750
2125 Ala Ala Leu Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val
2126         755             760             765
2128 Trp Tyr Val Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys
2129     770             775             780
2131 Val Tyr Phe Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly
2132 785             790             795             800
2134 Leu Gly Thr Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys
2135             805             810             815
2137 Asp Val Val Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu
2138             820             825             830
2140 Ala Ser Asn Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu
2141         835             840             845
2143 Thr Arg Leu Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe
2144     850             855             860
2146 Ala Asn Asp Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr
2147 865             870             875             880
2149 Glu Gly His Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val
2150             885             890             895
2152 Gln Ala Ser Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp
2153         900             905             910
2155 Val Asn Leu Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys
2156     915             920             925
2158 Phe Ser Pro Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu
2159     930             935             940
2161 Lys Val Pro Leu Leu Gly Val Ser Ser Pro Ser Ser Tyr Ser Glu His
2162 945             950             955             960
2164 Thr Ser Glu Ala Thr Ser Glu Gly Ser Ile Phe Glu Val Gly His Leu
2165             965             970             975
2167 His Leu Ala Val Asp Arg Asp Val Asn Gln Ala Gly Ser Lys Ile Lys
```

```
RAW SEQUENCE LISTING                    DATE: 10/02/2000
PATENT APPLICATION:  US/09/545,199A     TIME: 15:58:32

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Output Set: N:\CRF3\10022000\I545199A.raw

2168          980              985              990
2170 Ala Lys Tyr Thr Thr Gly Val Val Lys Gly Asn Phe Asn Thr Glu Ala
2171          995              1000.            1005
2173 Gly Lys Asn Ile Lys His Val Glu Lys Glu Glu Tyr Ser Ser Gln Leu
2174      1010             1015             1020
2176 Phe Ala Ser Ala His Ala Ser Gly Gly Gly Thr Ser Val Arg Tyr Asp
E--> 2177(025) 1025          1030             1035             1040
2179 Tyr Asn Ser Gln Asp Gly Gly Asn Ala Ser Val Gly Val Pro Thr Asn
2180          1045             1050             1055
2182 His Thr Gly Val Gly Ala Glu Ala Gly Met Ser Phe Thr His Thr Lys
2183          1060             1065             1070
2185 Asp Lys Glu Thr Leu Leu Thr His Thr Asn Ser Glu Leu Gln Val Lys
2186      1075             1080             1085
2188 His Gly Lys Leu His Val Leu Gly Tyr Ala Asp Ile Gly Gly Val Asp
2189      1090             1095             1100
2191 Ile Asn Thr Lys Leu Pro Glu Asp Ala Gln Ser Lys Ala Gln Lys Glu
E--> 2192(105) 1105          1110             1115             1120
2194 Ile Ala Ala Ser Lys Pro Glu Lys Thr Glu Gln Ser Ala Gln Asp Val
2195          1125             1130             1135
2197 Ala Gln Ala Gln Ser Asn Ala Asn Lys Asp Lys Glu Asn Lys Ala Pro
2198      1140             1145             1150
2200 Glu Ile Lys Glu Leu Ser Glu Ala Glu Ile Ala Asp Leu Met Ser Glu
2201      1155             1160             1165
2203 Lys Ser Lys Ala Tyr Phe Asp Phe Ala Glu Gln Ala Lys Lys Ala
2204      1170             1175             1180
2206 Pro Glu Asn Asn Arg Phe Glu Leu Ser Ala Lys Glu Ile Lys Ser Ser
E--> 2207(185) 1185          1190             1195             1200
2209 Lys Gln Lys Asp Gln Tyr Asp His Glu Ser Glu Arg Thr Thr Phe Lys
2210          1205             1210             1215
2212 Val Gly Pro Glu Ala Glu Ala His Ser Ala Val Ala Asp Met Val Ser
2213          1220             1225             1230
2215 His Leu Val Lys Glu Tyr Arg Asp Ala Gln Asn Gly Thr Lys Gln Asp
2216      1235             1240             1245
2218 Gly Thr Val Ala Leu Gln His Ala Ser Asp Val Leu Asn Ile Val Thr
2219      1250             1255             1260
2221 Gly Asp Leu Ala Gly Ser Ser Ala Lys Leu Ser Val Glu Arg Thr His
E--> 2222(265) 1265          1270             1275             1280
2224 Glu Thr Lys Arg Thr Thr Glu Thr Gly Gly Ile Val Thr Lys Ile Gly
2225          1285             1290             1295
2227 Gly Asn Val Thr Leu Ser Ala Arg Ser Gly Ser Val Asn Leu Lys Asn
2228          1300             1305             1310
2230 Val Gln Ser Asp Glu Gln Ala Asn Leu Thr Leu Arg Ala Lys Glu Asp
2231      1315             1320             1325
2233 Val Asn Val Leu Ser Gly Glu Lys Thr Arg Glu Thr Thr Glu Thr Val
2234      1330             1335             1340
2236 Ser Arg Gln Lys Leu Ser His Gly Val Asn Ala Gly Cys Ser Met Met
E--> 2237(345) 1345          1350             1355             1360
2239 Ser Gly Ala Cys Thr Ala Gly Val Ser Thr Ser Leu Glu Gly Asn Glu
2240      1365             1370             1375
```

When numbering the
first amino acid on
a line, begin the
number directly below
the first letter of
the amino acid

```
     2242 Ser Tyr Thr Ser Glu Arg Glu Thr Ala Gln Asn Asn Ser Phe Leu Lys
     2243          1380            1385            1390
     2245 Ala Arg Asn Met Lys Val Glu Ala Gly Arg Asp Phe Asn Val Val Ser
     2246          1395            1400            1405
     2248 Ser Asn Ile Asp Ala Asp Lys Leu Asp Leu His Val Lys Gly Lys Thr
     2249      1410            1415            1420
     2251 Asn Val Val Ser Lys Gln Asp Thr Leu Gln Lys Val Thr His Gly Val
E--> 2252 425            1430            1435            1440
     2254 Asp Tyr Asn Leu Ser Ala Gly Val Ala Leu Ser Ser Ala Thr Ile Ala
     2255          1445            1450            1455
     2257 Thr Pro Thr Gly Asn Val Gly Phe Gly Tyr Thr Asn Glu Thr Glu Ser
     2258          1460            1465            1470
     2260 Lys Arg Thr Val Asn Gln Gln Ala Gly Ile Lys Ala Asn Lys Ile Thr
     2261      1475            1480            1485
     2263 Gly Gln Thr His Asp Leu Asn Leu Glu Gly Gly Tyr Leu Val Ser Asn
     2264      1490            1495            1500
     2266 Asp Lys Asp Asn Gln Leu Lys Val Thr Gly Asp Val Thr Thr Lys Ala
E--> 2267 505            1510            1515            1520
     2269 Leu His Asp Gln His Asp Lys Asp Gly Gly Thr Phe Gly Leu Ser Val
     2270          1525            1530            1535
     2272 Gly Ile Ser Glu Arg Gly Thr Thr Ala Phe Asn Val Arg Gly Gly Arg
     2273          1540            1545            1550
     2275 Ala Glu Gln Lys His Tyr Asn Ala Thr Gln Lys Ser Thr Leu Ser Gly
     2276      1555            1560            1565
     2278 Val Asp Thr Ser Gln Ala Asn Val Ser Gly Gln Val Asn Thr Asp Leu
     2279      1570            1575            1580
     2281 Thr Lys Ala Lys Ala Val Thr Arg Asp Asp Thr Tyr Ala Ser Thr Gln
E--> 2282 585            1590            1595            1600
     2284 Phe Ser Phe Glu Val Ala Asp Ile Val Glu Leu Gly Gln Arg Ala Lys
     2285          1605            1610            1615
     2287 Asn Lys Leu Ser Ala Pro Asn Asn Asp Thr Asp Met Ala Ser Gly Ser
     2288          1620            1625            1630
     2290 Thr Leu Arg Ser Arg Ser Thr Thr Glu Glu Ala Asp Val Pro Thr Thr
     2291      1635            1640            1645
     2293 Arg Ser Arg Val Thr Asp Glu Ala Asp Ser Val Ser Val Lys Asn Pro
     2294      1650            1655            1660
     2296 Ile Tyr Glu Ser Ala Asp Ala Val Val Pro Thr Pro Arg Ser Arg Asn
E--> 2297 665            1670            1675            1680
     2299 Val Asp Ser Thr Asp Leu Val Asp Asn Pro Leu Tyr Ala Ser Ala Thr
     2300          1685            1690            1695
     2302 Thr Lys Ala Asn Ile His Asp Tyr Glu Glu Ile Pro Ala Val Tyr Ser
     2303          1700            1705            1710
     2305 Lys Val Gly Asp Asn Asn Ala Asp Leu Val Arg His Lys Thr Ala Thr
     2306      1715            1720            1725
     2308 Ser Asp Glu His Leu Tyr Ala Glu Ile Asn Glu Pro Thr Tyr Ser Arg
     2309      1730            1735            1740
     2311 Val Gly Asp Lys Asn Ala Asp Met Arg Arg His Asn Ala Ala Gly Thr
E--> 2312 745            1750            1755            1760
     2314 Thr Asp Tyr Ala Asp Val Val Gln Ala His Thr Arg Lys Ala Asp Asp
```

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          RAW SEQUENCE LISTING              DATE: 10/02/2000
          PATENT APPLICATION:  US/09/545,199A      TIME: 15:58:32

          Input Set : A:\6227.txt
          Output Set: N:\CRF3\10022000\I545199A.raw

     2315            1765            1770            1775
     2317 Pro Leu Pro Ala Leu Pro Asn Gln Gly Lys Ala Arg Thr Val Asn Asp
     2318            1780            1785            1790
     2320 Gly Ser Glu His Ile Tyr Thr Asp Ile Ser Asp Val Gly Thr Gln Thr
     2321       1795            1800            1805
     2323 Lys Ala Ile Asp Ser Thr Tyr Ala Thr Val Gly Met Pro Lys Ala Asn
     2324       1810            1815            1820
     2326 Ala Val Asn Leu Ile Gly Gln Asn Gly Leu Gly Ser Ile Tyr His Ser
E--> 2327 825            1830            1835            1840
     2329 Pro Asp Ser Ala Tyr Lys Thr Trp Gln Leu Leu Asp Gln Phe Ala Asn
     2330            1845            1850            1855
     2332 Lys Gly Gly Asp Ala Val Phe Leu Arg Pro Ala Thr Glu Met Lys Cys
     2333            1860            1865            1870
     2335 Ala Gly Ala Pro Leu Lys Tyr Thr Phe Ile Val Arg Asp Tyr Leu Leu
     2336       1875            1880            1885
     2338 Arg Arg His Thr Leu Asp Lys Ser Arg Leu Phe Tyr Asn Ala His Asn
     2339       1890            1895            1900
     2341 Lys Thr Leu Phe Ser Val Pro Ile Val Asp Ala Lys Val Lys Met Leu
E--> 2342 905            1910            1915            1920
     2344 Phe Ala Glu Lys Asn Ile Gln Val Asn Tyr Asp Arg Ser Leu Thr Ala
     2345            1925            1930            1935
     2347 Ile Asp Leu Ser Lys Arg Ile Ala Thr Phe Asn Ser Pro Glu Gly Val
     2348       1940            1945            1950
     2350 Val Glu Val Pro Tyr Asp Phe Ile Asn Val Val Pro Pro Met Arg Ala
     2351       1955            1960            1965
     2353 Pro Asp Ala Val Arg Gln Ser Ala Leu Ala Trp Gln Glu Gly Lys Trp
     2354      1970            1975            1980
     2356 Ala Asn Asp Gly Trp Val Glu Val Glu Lys His Thr Leu Arg His Arg
E--> 2357 985            1990            1995            2000
     2359 Arg Tyr Ala Asn Val Phe Ala Val Gly Asp Val Ala Gly Val Pro Lys
     2360            2005            2010            2015
     2362 Gly Lys Thr Ala Ala Ser Val Lys Trp Gln Val Pro Val Ala Val Ala
     2363       2020            2025            2030
     2365 His Leu Leu Ala Glu Leu Glu Gly Lys Pro Cys Asp Glu Ile Tyr Asn
     2366       2035            2040            2045
     2368 Gly Tyr Thr Ser Cys Pro Leu Ile Thr Gln Leu Gly Lys Gly Met Leu
     2369      2050            2055            2060
     2371 Val Glu Phe Asp Tyr Asn His Leu Thr Pro Ser Phe Pro Gly Val
E--> 2372 065            2070            2075            2080
     2374 Ile Ala Pro Leu Glu Glu Leu Trp Ala Thr Trp Ala Ile Lys Thr Leu
     2375            2085            2090            2095
     2377 Gly Leu Lys Pro Thr Tyr Leu Gly Met Leu Arg Gly Leu Ala
     2378       2100            2105            2110
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see following pages for more errors

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<210> 28
<211> 450
<212> PRT
<213> Pasteurella multocida

<400> 28
Ser Thr Lys Val Gly Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu
  1               5                  10                  15

Phe Leu Glu Asp Arg Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu
                20                  25                  30

Gly Leu Ser Asp Ala Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu
            35                  40                  45

Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr
        50                  55                  60

Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu
 65                  70                  75                  80

Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser
                85                  90                  95

Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr
            100                 105                 110

Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe
        115                 120                 125

Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe
        130                 135                 140

Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr
145                 150                 155                 160

Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met
                165                 170                 175

Asp Asp Ile Lys Ile Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg
            180                 185                 190

Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile
        195                 200                 205

Asn Arg Thr Gln Arg Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser
    210                 215                 220

Tyr Gln Leu Ser Leu Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala
225                 230                 235                 240

Tyr Arg Leu Ser Thr Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr
            245                 250                 255

Phe Glu Asp Arg Gly Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp
        260                 265                 270
```

(Handwritten margin notes: "entire sequence not shown"; "See item 10 on Error Summary Sheet"; "09/545,199A"; page "7"/"10")

Please Note: Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set : A:\6227.txt
Output Set: N:\CRF3\10022000\I545199A.raw

```
L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:118 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:2177 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
M:332 Repeated in SeqNo=16
L:3802 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:3803 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:3806 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:3807 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:3810 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:3811 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:3918 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:28
L:3918 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:3918 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:3918 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
L:3918 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
L:3921 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:28
L:3921 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:3921 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:3921 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
M:340 Repeated in SeqNo=28
L:3924 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:28
L:3924 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:28
L:3924 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:3924 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
L:5302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:5303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:5314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:5315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:5330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:5338 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:5386 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:36
L:5386 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:36
L:5386 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:36
L:5386 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:36
L:5386 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36
L:5389 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:36
L:5389 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:36
L:5389 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:36
L:5389 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:36
M:340 Repeated in SeqNo=36
L:5395 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:36
L:5395 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:36
L:5395 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:36
L:5395 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:36
L:5398 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:36
L:5398 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:36
L:5398 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:36
```

VERIFICATION SUMMARY   DATE: 10/02/2000
PATENT APPLICATION: US/09/545,199A   TIME: 15:58:35

Input Set : A:\6227.txt
Output Set: N:\CRF3\10022000\I545199A.raw

```
L:5398 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:36
L:5435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5436 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5451 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5483 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5485 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5534 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:38
L:5534 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:38
L:5534 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:38
L:5534 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:38
L:5534 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:38
L:5546 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:38
L:5546 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:38
L:5546 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:38
L:5546 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:38
M:340 Repeated in SeqNo=38
L:5659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:6585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:9138 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:10838 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:90
L:10838 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:90
L:10838 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:90
L:10840 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:90
L:10840 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:90
M:340 Repeated in SeqNo=90
L:11563 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:102
L:11564 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:102
L:11881 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:103
L:11881 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:103
L:11881 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:103
L:11881 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:103
L:11881 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:103
```